L3 ANSWER 17 OF 18 MEDLINE
ACCESSION NUMBER: 92276435 MEDLINE
DOCUMENT NUMBER: 92276435
TITLE: Co- ***amplification*** of specific sequences of ***HCV*** and ***HIV*** -1 genomes by using the polymerase chain reaction assay: a potential tool for the simultaneous ***detection*** of ***HCV*** and ***HIV*** -1.
AUTHOR: Nedjar S; Biswas R M; Hewlett I K
CORPORATE SOURCE: Laboratory of Hepatitis, Food and Drug Administration, Bethesda, Maryland 20892.
SOURCE: JOURNAL OF VIROLOGICAL METHODS, (1991 Dec) 35 (3) 297-304. Journal code: HQR. ISSN: 0166-0934.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199209
AB A rapid and simple method using the polymerase chain reaction (PCR) was devised for the co- ***amplification*** and simultaneous ***detection*** of hepatitis C virus (HCV) and human immunodeficiency virus type 1 (HIV-1) specific sequences in the same serum sample. Genomic RNA was extracted from 13 blood donor sera that were reactive in ELISA for both anti-HCV and anti-HIV-1. The extracted RNA was reverse transcribed into cDNA and ***amplified*** using nested primer pairs (SN01 and SN04; SN02 and SN03) based on the HCV prototype sequence of clones 37b and 81, and SK 38/39 for HIV-1 simultaneously. PCR products were analyzed by liquid hybridization or Southern blot hybridization with 32P end-labeled oligonucleotide probes from the regions between the primer pairs, excluding the primer sequences. HCV-RNA was ***detected*** in all 13 (100%) samples tested; HIV-RNA was ***detected*** in 11 (85%) samples. The ability to co- ***amplify*** specific sequences from two different viral genomes in the same reaction mixture offers the possibility of simultaneous ***detection*** and diagnosis of more than one viral agent in serum samples of infected individuals.

L3 ANSWER 16 OF 18 MEDLINE
ACCESSION NUMBER: 94088613 MEDLINE
DOCUMENT NUMBER: 94088613
TITLE: ***HIV*** -1 and ***HCV*** co-infected patients: ***detection*** of active viral expression using a nested polymerase chain reaction.
AUTHOR: Richard L; Pellegrin J L; Barbeau P; Brossard G; Leng B; Fleury H J
CORPORATE SOURCE: Laboratoire de Virologie, Universite de Bordeaux II, France.
SOURCE: MOLECULAR AND CELLULAR PROBES, (1993 Oct) 7 (5) 405-10. Journal code: NG9. ISSN: 0890-8508.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199403
AB The aim of the present study was to determine, in a population of 70 HIV-1 infected patients with antibodies to HCV, the percentages of individuals with an active replication of HIV-1, HCV or both. During a one year

follow-up of these patients at different stages of disease, blood samples were regularly collected for determination of transaminase, beta 2 microglobulin and CD4+ lymphocytes. Total RNAs were extracted from the sera, retrotranscribed with MoMuLV reverse transcriptase and nested PCR assays were carried out separately with sets of primers homologous to the 5' non-translated region of HCV and in HIV-1 gag. The ***amplified*** products were subjected to electrophoresis and observed under u.v. illumination after staining with ethidium bromide. For some samples, the identity of the ***amplified*** products was confirmed by Southern blotting by hybridization with enzyme-labelled probes. A total of 57% of the patients were found to produce HIV-1 RNA and 62% HCV RNA, while 34% produced both. HIV-1 RNA production was correlated with beta 2 microglobulin and CD4+ levels; active replication of HCV was correlated with hepatitis but not with CD4+ levels nor with HIV-1 RNA synthesis.

L3 ANSWER 5 OF 18 MEDLINE
ACCESSION NUMBER: 1999030780 MEDLINE
DOCUMENT NUMBER: 99030780
TITLE: PCR for HBV, ***HCV*** and ***HIV*** -1 experiences and first results from a routine screening programme in a large blood transfusion service.
AUTHOR: Schottstedt V; Tuma W; Bunger G; Lef evre H
CORPORATE SOURCE: Red Cross Blood Transfusion Service North-Rhine Westfalia, Germany.
SOURCE: BIOLOGICALS, (1998 Jun) 26 (2) 101-4.
Journal code: AMW. ISSN: 1045-1056.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199902
ENTRY WEEK: 19990204
AB We adapted the PCR method to screen up to 3000 blood donations per day for hepatitis B, hepatitis C and HIV-1 virus contamination. Up to 600 aliquots (average 418 donations) are pooled by using an automatic sample processor with disposable tips (validated to avoid contamination) taken from blood donations which are serologically negative and free for clinical usage according to federal regulations. In the case of a positive PCR pool result the viraemic donation is identified by two additional PCR pools testing steps with smaller pool sizes. All of the steps are supported by electronic data processing. After virus concentration by ultracentrifugation, and in the case of HCV and HIV-1 an additional reverse transcription step, PCR ***amplifications*** are performed. PCRs are done for each virus in two genomic regions. Laser-induced ***detection*** after PAGE and computer-analysis are used to identify the ***amplification*** products. Using this validated methodology routine we have checked 428 896 donations up to the end of August 1996. During this survey we found at least 24 viruses-containing donations which were negative in corresponding serological tests and would have been transfused (2 HBV-, 22 HCV-, 0 HIV-1 -containing donations). It seems possible for large transfusion centres to shorten the diagnostic window periods with our PCR-methodology with acceptable costs (15 DM per donation for all three viruses including logistics, developments and investments).


L3 ANSWER 2 OF 18 MEDLINE

ACCESSION NUMBER: 1999330468 MEDLINE
DOCUMENT NUMBER: 99330468
TITLE: Screening for HBV, ***HCV*** and ***HIV*** genomes in blood donations: shortcomings of pooling revealed by a multicentre study simulating real-time testing.
AUTHOR: Lefr`ere J J; Cantaloube J F; Defer C; Mercier B; Loiseau P; Vignon D; Pawlotsky J M; Biagini P; Lerable J; Rouger P; Roudot-Thoraval F; Ferec C
CORPORATE SOURCE: Institut National de la Transfusion Sanguine, Paris, France.. lefrere@worldnet.fr
SOURCE: JOURNAL OF VIROLOGICAL METHODS, (1999 Jun) 80 (1) 33-44. Journal code: HQR. ISSN: 0166-0934.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
(MULTICENTER STUDY)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199911
ENTRY WEEK: 19991104
AB This study was undertaken in order to determine whether screening of viremic blood donations by testing of pooled donor samples could constitute a technically feasible transfusional safety measure. A pilot study of real-time simulation, on a day-to-day basis, of screening of three viral genomes (hepatitis B virus (HBV), hepatitis C virus (HCV) and human immunodeficiency virus (HIV)) was conducted by five French Blood Centers on plasma samples collected from blood donors and studied within undiluted samples and within sample pools of various sizes. This study was carried out within time conditions compatible with the release of platelets. For the ***detection*** of HCV and HIV genomes, the five laboratories achieved a sensitivity that decreased with the size of the sample pool. Four were successful in ***detecting*** all undiluted samples. In the 1/10 diluted samples, four failed to ***detect*** one HIV or HCV sample. In the 1/100 diluted samples, all laboratories failed to ***detect*** one or more HIV or HCV samples. For HBV genome, no participating laboratories ***detected*** all of the samples of the panel, even undiluted samples, and the sample pooling considerably affected sensitivity. The improvement and standardization of assays needs to be attained, and training of laboratories appears to be a step crucial for routine screening of viral genomes in blood donations.

=> d his

(FILE 'HOME' ENTERED AT 15:12:50 ON 01 DEC 2000)

FILE 'MEDLINE' ENTERED AT 15:12:56 ON 01 DEC 2000
L1 5541 S (HIV OR HCV)/TI AND (AMPLIF? OR DETECT?)
L2 28 S (HIV AND HCV)/TI AND (AMPLIF? OR DETECT?)
L3 18 S (HIV (3A) HCV)/TI AND (AMPLIF? OR DETECT?)

AB Resistance to activated protein C is the most common hereditary cause of thrombophilia and is significantly linked to factor V Leiden. We designed **primers** in order to identify factor V Leiden by allele-specific PCR amplification. Amplification specificity for factor V was ensured by a 3' **primer** located at the intron 9/exon 10 border of the gene. One sense and two antisense **primers** were used in two separate **primer** mixes specific for factor V ARG506 (wild-type) or factor V GLN506 (factor V Leiden). In each PCR reaction a pair of **primers** amplifying a fragment of the human growth hormone gene was included as an internal positive amplification control. The presence or absence of specific PCR amplification allowed definite allele assignment without the need for any postamplification specificity step. The **internal positive control primers** indicate a successful PCR amplification, allowing the assignment of homozygosity. In a prospective study 126 patients with thromboembolic events were analyzed using this technique and PCR-RFLP. The concordance between these methods was 100%. In 27 patients a heterozygous factor V GLN506 mutation was detected, whereas 1 patient with recurrent thromboembolism was homozygous. No false-positive or false-negative results were observed in the homozygous as well as heterozygous samples. Additionally, in 15 samples identified to carry the point mutation by allele-specific PCR amplification, automatic sequencing has confirmed the heterozygous or homozygous point mutation. Due to its time- and cost-saving features allele-specific amplification should be considered for screening of factor V Leiden.

L6 ANSWER 20 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 12
ACCESSION NUMBER: 1995:490904 BIOSIS
DOCUMENT NUMBER: PREV199598505204
TITLE: Improved polymerase chain reaction (PCR) detection of Gaeumannomyces graminis including a safeguard against false negatives.
AUTHOR(S): Ward, Elaine
CORPORATE SOURCE: Plant Pathol. Dep., IACR, Rothamsted, Harpenden, Herts AL5 2JQ UK
SOURCE: European Journal of Plant Pathology, (1995) Vol. 101, No. 5, pp. 561-566.
ISSN: 0929-1873.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A previously reported method for polymerase chain reaction (PCR) detection of Gaeumannomyces graminis was modified to simplify it, improve its specificity and decrease the possibility of contamination of the assay. The modified method also allowed discrimination between the G. graminis varieties (tritici and avenae) that are pathogenic to wheat and oats respectively and the variety weakly pathogenic to wheat (var. graminis). An **internal positive control** for the PCR was also added to the test by including a second pair of **primers** in the reaction. This positive control has wider application in PCR tests for detection of other fungi.

L1 ANSWER 1 OF 1 MEDLINE
ACCESSION NUMBER: 1998019514 MEDLINE
DOCUMENT NUMBER: 98019514
TITLE: Allele-specific **PCR** amplification of factor V **Leiden** to identify patients at risk for **thromboembolism**.
AUTHOR: Blasczyk R; Wehling J; Ritter M; Neubauer A; Riess H
CORPORATE SOURCE: Department of Internal Medicine, Virchow-Klinikum, Humboldt-Universitat zu Berlin, Germany.
SOURCE: BEITRAGE ZUR INFUSIONSTHERAPIE UND TRANSFUSIONSMEDIZIN, (1997) 34 236-41.
Journal code: B7I. ISSN: 1023-2028.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199803
ENTRY WEEK: 19980301

AB Resistance to activated protein C is the most common hereditary cause of thrombophilia and is significantly linked to factor V Leiden. We designed primers in order to identify factor V Leiden by allele-specific PCR amplification. Amplification specificity for factor V was ensured by a 3' primer located at the intron 9/exon 10 border of the gene. One sense and two antisense primers were used in two separate primer mixes specific for factor V ARG506 (wild-type) or factor V GLN506 (factor V Leiden). In each PCR reaction a pair of primers amplifying a fragment of the human growth hormone gene was included as an internal positive amplification control. The presence or absence of specific PCR amplification allowed definite allele assignment without the need for any postamplification specificity step. The internal positive control primers indicate a successful PCR amplification, allowing the assignment of homozygosity. In a prospective study 126 patients with thromboembolic events were analyzed using this technique and PCR-RFLP. The concordance between these methods was 100%. In 27 patients a heterozygous factor V GLN506 mutation was detected, whereas 1 patient with recurrent thromboembolism was homozygous. No false-positive or false-negative results were observed in the homozygous as well as heterozygous samples. Additionally, in 15 samples identified to carry the point mutation by allele-specific PCR amplification, automatic sequencing has confirmed the heterozygous or homozygous point mutation. Due to its time- and cost-saving features allele-specific amplification should be considered for screening of factor V Leiden.